RECEIVED
CENTRAL FAX CENTER
DEC 0 9 2005

Amendments to the Claims

Claims 1-2 (Cancelled).

Claim 3 (Currently amended): A method of determining whether a compound modulates insulin receptor activity, comprising comparing using a processor all or part of the structure of the compound to all or part of the fitted quaternary structure of insulin receptor to determine ~~whether~~ how the compound interacts with the insulin receptor, the comparing step comprising:

~~a)~~ providing a computer program on the processor, the computer program including structural coordinates defining a ligand binding site conformation including at least one residue from monomer A in Table 1 and at least one residue from monomer B in Table 1, the ligand binding site defined by the approximate amino acid intersidechain distances listed in Table 1[[,]]; ~~wherein~~ the program ~~displays~~ displaying all or part of the fitted quaternary structure of the insulin receptor including the ligand binding site;

~~b)~~ comparing the structural coordinates of the compound to the structural coordinates of the ligand binding site and determining whether the compound fits spatially into the ligand binding site;

wherein if the compound fits spatially into the ligand binding site, next determining whether the ~~test~~ compound modulates insulin receptor activity by determining if the ~~test~~ compound agonizes insulin receptor activity in an insulin receptor activity assay.

Claims 4-5 Cancelled

Claim 6 (Previously presented): The method of claim 3, wherein the fitted quaternary structure of insulin receptor comprises substantially the entire fitted quaternary structure of insulin receptor.

Claims 7-8 (Cancelled).

Claim 9 (Currently amended): A method of determining whether a compound modulates insulin receptor activity, comprising comparing using a processor all or part of the structure of the compound to all or part of the fitted quaternary structure of insulin receptor to determine how the compound interacts with the insulin receptor, the comparing step comprising:

~~a)~~ providing a computer program on the processor, the computer program including structural coordinates defining a ligand binding site conformation including at least one residue from monomer A in Table 1 and at least one residue from monomer B in Table 1, the ligand binding site defined by the approximate amino acid ~~coordinates~~ intersidechain distances listed in Table 1[[,]]; ~~wherein~~ the program ~~displays~~ displaying all or part of the fitted quaternary structure of the insulin receptor including the ligand binding site;

~~b)~~ comparing the structural coordinates of the compound to the structural coordinates of the ligand binding site and determining whether the compound fits spatially into the ligand binding site;

wherein if the compound fits spatially into the ligand binding site, next determining whether the ~~test~~ compound modulates insulin receptor activity by determining whether the ~~test~~ compound antagonizes insulin receptor activity in an insulin receptor activity assay.

Claim 10 (Cancelled).

Claim 11 (Currently amended): A method of determining whether a compound modulates insulin receptor activity, comprising comparing using a processor all or part of the structure of the compound to all or part of the fitted quaternary structure of insulin receptor to determine how the compound interacts with the insulin receptor, the comparing step comprising:

~~a)~~ providing a computer program on the processor, the computer program including structural coordinates including at least one residue from between amino acids 250 to 280 of ~~SEQ ID NO:16~~ Figure 12 and at least one residue from the L1 surface in Table 2[[,]]; ~~wherein~~ the program ~~displays~~ displaying all or part of the fitted quaternary structure of the ~~ligand binding site~~insulin receptor including the residues;

~~b)~~ comparing the structural coordinates of the compound to the structural coordinates of ~~at least one residue between amino acids 250 to 280 of SEQ ID NO:16~~ the residues and determining whether the compound interacts with the ~~residue~~residues;

wherein if the compound fits spatially between the residues, next determining whether the ~~test~~ compound modulates insulin receptor activity by determining whether the ~~test~~ compound agonizes insulin receptor activity in an insulin receptor activity assay.

Claim 12 (Cancelled).

Claim 13 (Currently amended): A method of determining whether a compound modulates insulin receptor activity, comprising comparing using a processor ~~to compare~~ all or part of the

structure of the compound to all or part of the fitted quaternary structure of insulin receptor to determine how the compound interacts with the insulin receptor, the comparing step comprising:

~~a)~~ providing a computer program on the processor, the computer program including structural coordinates including at least one residue between amino acids 250 to 280 of ~~SEQ ID NO:16~~ Figure 12 and at least one residue from the L1 surface in Table 2[[,]]~~wherein~~; the program ~~displays~~ displaying all or part of the fitted quaternary structure ~~thereof~~of the insulin receptor including the residues;

~~b)~~ comparing the structural coordinates of the compound to the structural coordinates of the ~~at least one residue between amino acids 250 to 280 of SEQ ID NO:16~~ residues and determining whether the compound interacts with the ~~residue~~residues;

wherein if the compound fits spatially between the residues, next determining whether the ~~test~~ compound modulates insulin receptor activity by determining whether the ~~test~~ compound antagonizes insulin receptor activity in an insulin receptor activity assay.

Claim 14 (Cancelled).

Claim 15 (Previously presented): The method of claim 3, wherein the insulin receptor is bound to insulin.

Claims 16-19 (Cancelled).

Claim 20 (Previously presented): The method of claim 9, wherein the insulin receptor is bound to insulin.

Claim 21 (Previously presented): The method of claim 11, wherein the insulin receptor is bound to insulin.

Claim 22 (Previously presented): The method of claim 13, wherein the insulin receptor is bound to insulin.

Claim 23 (Currently amended): The method of claim 11, wherein the at least one residue between amino acids 250 to 280 of ~~SEQ ID NO:16~~ Figure 12 comprises at least one residue selected from the group consisting of Lys265, Lys267, Asn268, Arg270, Arg271 and Gln272.

Claim 24 (Currently amended): The method of claim 13, wherein the at least one residue between amino acids 250 to 280 of ~~SEQ ID NO:16~~ Figure 12 comprises at least one residue selected from the group consisting of Lys265, Lys267, Asn268, Arg270, Arg271 and Gln272.

Claim 25 (Cancelled)